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ALLEN, MARIANNE P	

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BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

Application Number: 09/976,054
Filing Date: October 15, 2001
Appellant(s): CHEIKH ET AL.

Holly Logue Prutz
For Appellant

EXAMINER'S ANSWER

This is in response to the appeal brief filed 5/1/2008 appealing from the Office action mailed 11/13/2007.

(1) Real Party in Interest

A statement identifying by name the real party in interest is contained in the brief.

(2) Related Appeals and Interferences

The examiner is not aware of any related appeals, interferences, or judicial proceedings which will directly affect or be directly affected by or have a bearing on the Board's decision in the pending appeal.

(3) Status of Claims

The statement of the status of claims contained in the brief is correct.

(4) Status of Amendments After Final

The appellant's statement of the status of amendments after final rejection contained in the brief is correct.

(5) Summary of Claimed Subject Matter

The summary of claimed subject matter contained in the brief is correct.

(6) Grounds of Rejection to be Reviewed on Appeal

The appellant's statement of the grounds of rejection to be reviewed on appeal is correct.

(7) Claims Appendix

The copy of the appealed claims contained in the Appendix to the brief is correct.

(8) Evidence Relied Upon

5,777,018	MOFFATT ET AL	6-1998

Xing et al., "Cloning a second form of adenine phosphoribosyl transferase gene (*TaAPT2*) from wheat and analysis of its association with thermo-sensitive genic male sterility (TSGMS)." Plant Science, Vol. 169, 2005, pp. 37-45.

Genbank Accession No. U22442, 8 November 1995, Triticum aestivum (bread wheat).

(9) Grounds of Rejection

The following ground(s) of rejection are applicable to the appealed claims:

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 20-23 and 25 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a new matter rejection.

Claims 20-23 and 25 are not originally filed claims. They were introduced in the amendment filed 7/21/2006. These claims were withdrawn as being directed to a non-elected invention in the Office action dated 9/27/2006 and rejoined for examination in the Office action dated 3/6/2007.

Claim 20 is directed to a transformed plant. It depends on allowed claim 12 reciting SEQ ID NO: 5. Claim 21 is directed to a transformed host cell. Claim 22 specifies that the host cell is a plant cell. Claim 23 is directed to a transformed plant comprising the host cell of claim 21. Claim 25 is directed to a transformed plant consisting of host cells of claim 21.

Basis was first stated to be "throughout the specification and in the claims as originally filed, for example, on page 36, lines 8-9, page 40, lines 12-14, and page 44, lines 8-15." (See appellant's 7/21/06 response.) Page 36, lines 8-9; page 40, lines 12-14; and page 44, lines 8-15, do not disclose transformed host cells or transformed plants.

Original claims 6, 7, and 11 filed 10/15/2001 are reproduced below and italicized:

6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for adenine phosphoribosyl transferase or fragment thereof;

(b) a nucleic acid sequence which encodes for [3 glucosidase or fragment thereof; and

(c) a nucleic acid sequence which encodes for isopentyltransferase or fragment thereof;

(d) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (c); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7. The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (c).

11. A method of producing a plant containing an overexpressed protein comprising:

(A) transforming said plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein said promoter region is linked to a structural region, wherein said structural region has a nucleic acid sequence selected from group consisting of SEQ ID NO: 1 through SEQ ID NO: 711 wherein said structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein said functional nucleic acid molecule results in overexpression of the protein; and

(B) growing said transformed plant.

These original claims clearly contemplate and disclose plants transformed with nucleic acid molecules operably linked to regulatory sequences and that express a protein.

None of claims 20-23 and 25 requires that the nucleic acid be in association with regulatory sequences such as promoters and transformed plants having nucleic acid sequences in the absence of such regulatory sequences are not disclosed.

Basis was then stated to be at page 82, line 18, to page 105, line 3, of the specification. (See appellant's 6/6/07 response.) These pages of the specification form a section titled **Plant Constructs and Plant Transformants**. This section describes the production of plant constructs and plant transformants for the purpose of expressing or overexpressing a protein of interest. That is, the plant construct or plant transformant must be capable of producing the encoded protein. In particular, page 83, lines 16-17, ("Exogenous genetic material may be transferred into a plant cell and the plant cell by the use of a DNA vector or construct designed

for such a purpose…") and page 88, line 20, ("A vector or construct may also include regulatory elements…") were pointed to as basis for the claims.

The full paragraphs from page 83 are reproduced below and italicized.

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the present invention may be overexpressed in a transformed cell or transformed plant. Particularly, any of the cytokinin pathway proteins or fragments thereof may be overexpressed in a transformed cell or transgenic plant. Such overexpression may be the result of transient or stable transfer of the exogenous genetic material.

Exogenous genetic material may be transferred into a plant cell and the plant cell by the use of a DNA vector or construct designed for such a purpose. Design of such a vector is generally within the skill of the art (See, Plant Molecular Biology: A Laboratory Manual, Clark (ed.), Springier, New York (1997), the entirety of which is herein incorporated by reference).

The full paragraphs from pages 88-89 are reproduced below and italicized.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac et al., Plant Mol. Biol. 25:587-596 (1994), the entirety of which is herein incorporated by reference). Expression in root tissue could also be

accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have been identified (Lamet al., Proc. Natl. Acad. Sci. (US.AS 86:7890-7894 (1989), herein incorporated by reference in its entirety). Other root cell specific promoters include those reported by Conkling et al. (Conkling et al., Plant Physiol. 93:1203-1211 (1990), the entirety of which is herein incorporated by reference).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619; 5,391,725; 5,428,147; 5,447,858; 5,608,144; 5,608,144; 5,614,399; 5,633,441; 5,633,435; and 4,633,436, all of which are herein incorporated in their entirety. In addition, a tissue specific enhancer may be used (Fromm et al., The Plant Cell 1:977-984 (1989), the entirety of which is herein incorporated by reference).

Constructs or vectors may also include with the coding region of interest a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the NOS 3' sequence (Ingelbrecht et al., The Plant Cell 1:671-680 (1989), the entirety of which is herein incorporated by reference; Bevan et al., Nucleic Acids Res. 11:369-385 (1983), the entirety of which is herein incorporated by reference), or the like.

A vector or construct may also include regulatory elements. Examples of such include the Adh intron 1 (Callis et al., Genes and Develop. 1:1183-1200 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase intron (Vasil et al., Plant Physiol. 91:1575-1579 (1989), the entirety of which is herein incorporated by reference) and the TMV omega element (Gallie et al., The Plant Cell 1:301-311 (1989), the entirety of which is herein

incorporated by reference). These and other regulatory elements may be included when appropriate.

When the specific lines of the specification pointed to as basis for the newly introduced claims are read in context of the whole disclosure, it is clear that transformed host cells and transformed plants containing the isolated polynucleotide alone (that is, not operably linked to other sequences needed for expression of the encoded polypeptide) are **not** contemplated. The use of "may" is not indicating that sequences needed for expression are optional or can be omitted, rather the use of "may" is indicating the variety of choices for those sequences.

A fair reading of the specification, including the originally filed claims, would readily convey to one of ordinary skill in the art that transformed host cells and transformed plants that have regulatory features for expression operably linked to the polynucleotide of interest would have been contemplated. Pages 83-105 are concerned with expression of sequences. These sequences would need to be in the context of regulatory sequences such as promoters. The specification does not disclose the inclusion of sequences, particularly SEQ ID NO: 5, in a plant where they are not intended to be expressed and/or not in a construct suitable for that purpose.

Finally, claims 21-22 are directed to a transformed host cell that is not required to be isolated. As such, these claims embrace transgenic organisms. Claim 21 is not limited to a plant but encompasses any organism. Non-plant transgenic organisms are not contemplated. Claim 25 is directed to a transformed plant consisting of a single type of transformed host cell. In

addition, the transformed plant of claim 25 consists of the transformed host cells of claim 21 which are not limited to plant cells. A plant of this type is not disclosed nor contemplated.

Claims 20-23 and 25 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. This is an enablement rejection.

SEQ ID NO: 5 is a 440 nucleotide sequence isolated from Zea mays or maize. Table A on page 208 of the specification identifies SEQ ID NO: 5 as a maize adenine phosphoribosyl transferase. It was isolated from the LIB3061 cDNA library. Page 169 of the specification also identifies this library as CMz035. The library was generated from maize endosperm tissue at the V10+ plant development stage. SEQ ID NO: 5 is disclosed as having sequence similarity to NCBI GI 726304. GI 726304 corresponds to Accession No. U22442. This sequence is from Triticum aestivum (bread wheat). The length of this sequence is 845 nucleotides and the coding region is identified as being from nucleotides 48-593. The sequence encodes an adenine phosphoribosyltransferase. Alignment of SEQ ID NO: 5 with this sequence shows a query match of 28% and best local similarity of 66%. (See following page.)

Alignment of SEQ ID NO: 5 with Accession No. U22442.

```
TAU22442
LOCUS       TAU22442                845 bp    mRNA    linear   PLN 08-NOV-1995
DEFINITION  Triticum aestivum adenine phosphoribosyltransferase form 1 (APT1)
            mRNA, complete cds.
```

```
ACCESSION   U22442
VERSION     U22442.1  GI:726304
KEYWORDS    .
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 845)
  AUTHORS   Moffatt,B.A., Schnorr,K., Gaillard,C., Biget,E. and Laloue,M.
  TITLE     Nucleotide sequence of a wheat cDNA encoding Adenine
            Phosphoribosytransferase (GenBank U22442)(PGR95-030)
  JOURNAL   Plant Physiol. 108 (4), 1748 (1995)
REFERENCE   2  (bases 1 to 845)
  AUTHORS   Schnorr,K.S., Moffatt,B.A., Biget,E. and Laloue,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-1995) Kirk Matthew Schnorr, Department of
            Biological Chemistry, Institute of Molecular Biology, University of
            Copenhagen, Solvgade 83, Copenhagen K, DK 1307, Denmark



FEATURES             Location/Qualifiers
     source          1. .845
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /strain="Capitol"
                     /db_xref="taxon:4565"
                     /tissue_type="immature seeds"
                     /dev_stage="23 days after flowering"
     gene            1. .845
                     /gene="APT1"
     5'UTR           <1. .47
                     /gene="APT1"
     CDS             48. .593
                     /gene="APT1"
                     /EC_number="2.4.2.7"
                     /function="converts adenine to AMP"
                     /note="APRT"
                     /codon_start=1
                     /product="adenine phosphoribosyltransferase form 1"
                     /protein_id="AAA80609.1"
                     /db_xref="GI:726305"
                     /translation="MASDGRVERIASSIRAIPNFPKPGILFQDITTLLLDPQAFRDTT
                     DLFVERYKDKDITVVAGVEARGFIFGPPIALAIGAKFVPIRKPKKLPGEVISEEYSLE
                     YGTDKIEMHVGAVQPNDRVLIVDDLIATGGTLCAAAKLIERVGAKVVECACVIELPEL
                     KGRDKLGDMPVFVLVQADESV"
     3'UTR           594. .845
                     /gene="APT1"
     polyA_site      845
                     /gene="APT1"
                     /note="20 A nucleotides"
ORIGIN

 Query Match             28.0%;  Score 123.2;  DB 8;  Length 845;
  Best Local Similarity   66.1%;  Pred. No. 2.2e-18;
  Matches  211;  Conservative    0;  Mismatches  101;  Indels    7;  Gaps    4;

Qy          77 GCAGGCGAGGGCAGGCGGTGGTGGCGATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCG 136
               || ||||||||  ||||| ||| |||||||| | |   || | |||| ||| |  |||||
Db          22 GCGGGCGAGGGTCGGCGGCGGTTGCGATGGCATCC---GACGGGCGCGTGGAGCGGATCG 78

Qy         137 NCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATGTTTCAGGACATCA 196
                 |||  |||||  |  || ||| |||| || ||||||||||||  |||||||||||||||
Db          79 CGTCCAGCATCCGCGCCATCCCCAACTTCCCCAAGCCAGGGATTTTGTTTCAGGACATCA 138

Qy         197 NGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAACATATACCATTTTGTCAAGCGGT 256
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Db        139 CAACCTTGCTTCTCGATCCGCAGGCATTCCGTGACACCACTGACCTCTTTGTCGAGCGGT 198

Qy        257 ACAAGGACCAAGGNATCACCNTGGAAANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGA 316
              |||||||| |||  || ||  | |     | || ||| |||| |||||  ||| ||| ||
Db        199 ACAAGGACAAAGACATAACTGTAGTTGCT-GGTGTTGAAGCCAGAGGATTCATTTTTGGT 257

Qy        317 ACAACTANNTCTTANAANNAATTGGTCAAAAATNGGTGNCNATTGAGGAAGCNNAATNAG 376
              |  | |   |  |  |   || |||  ||| |  ||  | | | |||||||  ||  |
Db        258 CCTCCCATTGC--ATTAGCCATAGGTGCAAAGTTTGT-TCCAATAAGGAAGCCGAAAAAA 314

Qy        377 NTGCCANGCNAAATGATTT 395
              | ||  |  |  |||| |
Db        315 TTACCTGGTGAGGTGATAT 333
```

Xing et al. (Plant Science, 169:37-45, 2005) is not prior art but discloses sequences of adenine phosphoribosyl transferases from a variety of plants. Maize is not included. However, Accession No. U22442 sequence from wheat, Accession No. AI522952 from soybean, and Accession No. X58640 from Arabidopsis thaliana (see U.S. Patent No. 5,770,718 to Moffatt, of record) are discussed. These sequences would have been known prior to the effective filing date of the instant application. Sequence comparisons and phylogenic analysis were performed. The conserved amino acid residues among six sequences from four different plants, including wheat and Arabidopsis, are set forth. (See abstract, page 38 at section 2.2, page 44 and Figures 2 and 3.)

When SEQ ID NO: 5 is translated beginning at nucleotide 103 and aligned with the wheat amino acid sequence, the encoded maize amino acid sequence with the best alignment is set forth on the following page. Note that the wheat sequence is not bolded (top sequence) and the sequence encoded by SEQ ID NO: 5 is bolded (bottom sequence). **Note that the * indicates the presence in SEQ ID NO: 5 of an additional nucleotide that would result in a frame shift.** This nucleotide has been considered a cloning error for purposes of producing the best amino acid alignment. Note that the **$** indicates the presence in SEQ ID: 5 of an additional codon "gct" for Ala (see amino acids 1-5 in the alignment). Note that "Xaa" indicates at least

one unknown nucleotide in this triplet codon from SEQ ID NO: 5 such that multiple amino acids could be encoded. Note that + indicates highly conserved residues in the plant adenine phosphoribosyl transferases aligned by Xing et al. Appellant is reminded that when nucleotide sequences are translated into proteins, the intended amino acid in the protein is indicated by a codon of three nucleotides. If a number of nucleotides are inserted or deleted into the base nucleotide sequence and that number is not a multiple of three, a frame shift mutation occurs. A frame shift mutation results in some triplet codons being read incorrectly during translation. That is, the wrong amino acids are added to the protein and an alternative protein is produced. Translation of SEQ ID NO: 5 would result production of an alternative protein that is **not** an adenine phosphoribosyl transferase.

```
Met Ala Ser Asp Gly Arg Val Glu Arg Ile Ala Ser Ser Ile Arg Ala Ile Pro Asn
            +       +               +               +               +
Met Ala Ser$Asp Ala Arg Leu Ala Xaa Ile Xaa Ser Xaa Ile Xaa Val Xaa Pro Asp


Phe Pro Lys Pro Gly Ile Leu Phe Gln Asp Ile Thr Thr Leu Leu Leu Asp Pro Gln
     +   +       +           +           +
Xaa Pro Lys Pro Gly Xaa Met Phe Gln Asp Ile Xaa Xaa Xaa Xaa Xaa Phe Asp Pro Lys


Ala Phe Arg Asp Thr Thr Asp Leu Phe Val Glu Arg Tyr Lys Asp Lys Asp Ile Thr
                                  +   +       +   +                   +
Ala Xaa Arg Asp Asn Ile Tyr His Phe Val Lys Arg Tyr Lys Asp Gln Gly Ile Thr


Val  * Val Ala Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu
```

```
                  +           +   +   +           +   +

Xaa  g Lys Xaa Gly Val Lys Ala Arg Gly Xaa Xaa Phe Gly Thr Thr Xaa Ser Xaa


Ala Ile Gly Ala Lys --- Phe Val Pro Ile Arg Lys Pro Lys Lys Leu Pro Gly Glu
                  +                         +   +                   +

Xaa Xaa Leu Val Lys Asn Xaa Xaa Xaa Leu Arg Lys Xaa Asn Xaa Xaa Pro Xaa Xaa


Val Ile
     +
Met Ile
```

In view of this information, particularly the degree of amino acid sequence similarity between the wheat and Arabidopsis sequences known in the prior art, one of ordinary skill in the art would not have doubted that **SEQ ID NO: 5 encoded part** of a maize adenine phosphoribosyl transferase. However, it is clear that **SEQ ID NO: 5 does not encode the complete sequence** for the maize adenine phosphoribosyl transferase. The wheat sequence is 181 amino acids in length and the Arabidopsis sequence is 183 amino acids in length. In view of the nucleotide in SEQ ID NO: 5 that would result in a frame shift, SEQ ID NO: 5 can only be considered to encode approximately 59 amino acids of the maize adenine phosphoribosyl transferase. If SEQ ID NO: 5 was expressed, 59 amino acids of the maize adenine phosphoribosyl transferase fused to a random, not naturally occurring amino acid sequence would be produced due to the frameshift present in the nucleic acid sequence. A complete adenine phosphoribosyl transferase would not result.

For those claim embodiments that merely require the presence of the nucleic acid in the host cell or plant but not in a context or form where any protein is expressed, **the specification does not teach how to use** such transformed host cells or plants. The disclosure is directed to expressing or overexpressing sequences of interest in plants. For those claim embodiments that encompass the nucleic acid in the host cell or plant in a context or form where a protein may be expressed, the nucleic acid of claim 12 does not encode a complete or biologically active protein. The **specification does not teach how to use** such a transformed host cells or plants.

It is noted that the specification does not provide any example of a transformed host cell or plant having the sequence of SEQ ID NO: 5.

(10) Response to Argument

In section 7(B) of the brief appellant argues that claims 20-23 and 25 have basis throughout the specification and claims. This is not agreed with.

Claims 20-23 and 25 are not originally filed claims.

35 U.S.C.132 states that no amendment shall introduce new matter into the disclosure of the invention. The written description requirement prevents claiming subject matter that was not adequately described in the specification as filed. New or amended claims which introduce elements or limitations which are not supported by the as-filed disclosure violate the written description requirement. Claims 20-23 and 25 as newly introduced and as subsequently amended introduce concepts not contemplated by the originally filed claims and disclosure.

Original claims 6, 7, and 11 recite plants transformed with nucleic acid molecules operably linked to regulatory sequences and that express a protein. This language is paralleled on pages 22-24 of the specification as the contemplated invention. None of claims 20-23 and 25 requires that the nucleic acid be in association with regulatory sequences such as promoters and/or that the transformed plants express the recited nucleic acid sequence.

When the portions of the specification relied upon by appellant as providing basis for the newly introduced claims are read in context of the whole disclosure, it is clear that transformed host cells and transformed plants containing the polynucleotide operably linked to other sequences needed for expression of the encoded polypeptide are contemplated. The whole focus of the section on transformed plants at pages 82-105 of the specification is disclosure of sequences such as promoters and techniques that will result in the expression of the polynucleotide of interest. Transformed host cells and transformed plants containing the isolated

polynucleotide in the absence of such sequences are **not** contemplated. The use of "may" is not indicating that sequences needed for expression are optional or can be omitted, rather the use of "may" is indicating the variety of choices for those sequences.

Appellant's arguments do not address that claims 21-22 are directed to a transformed host cell that is not required to be isolated. As such, these claims embrace transgenic organisms. Claim 21 is not limited to a plant but encompasses any organism. Non-plant transgenic organisms are not contemplated. Claim 25 is directed to a transformed plant consisting of a single type of transformed host cell. In addition, the transformed plant of claim 25 consists of the transformed host cells of claim 21 which are not limited to plant cells. A plant of this type is not disclosed nor contemplated.

For all of these reasons, the claims as written constitute new matter.

In section 7(C) of the brief appellant argues that claims 20-23 and 25 are enabled by the specification. This is not agreed with. Appellant's arguments focus on how to make the claimed transformed host cells and transformed plants. This is not the basis of the enablement rejection and these arguments are not germane. The basis of the rejection is **how to use** the claimed transformed host cells and transformed plants. With respect to appellant's arguments on overexpressing the nucleic acid molecules, the claims do not require any expression nor do they require any sequences (such as promoters operably linked to SEQ ID NO: 5) that would result in expression.

Appellant's arguments do not address **how to use** the claimed transformed host cells and transformed plants **in the absence of any expression**. Even if the claims recited such

limitations, the enablement rejection set forth above makes clear that SEQ ID NO: 5 would not have been expected to produce a protein with biological activity. While appellant argues that nucleic acids that do not encode complete proteins or do not encode proteins at all (such as promoters) have well recognized utility (see the paragraph bridging pages 14-15 of the brief), neither the specification nor the brief discloses how to use a transformed host cell or transformed plant containing SEQ ID NO: 5 which does not encode a complete adenine phosphoribosyl transferase but rather a protein with a frameshift mutation. The brief fails to indicate what the well-recognized utility of the transformed host cell or transformed plant would be when SEQ ID NO: 5 is present. Appellant's arguments are general. They do not specifically address SEQ ID NO: 5 and what is known about this specific sequence. Appellant's arguments repeatedly assert that one of ordinary skill in the art would know how to make and use the claimed invention without disclosing how one of ordinary skill in the art would use the claimed transformed cells and transformed plants.

For all of these reasons, the specification fails to enable how to use the claimed transformed cells and transformed plants.

(11) Related Proceeding(s) Appendix

No decision rendered by a court or the Board is identified by the examiner in the Related Appeals and Interferences section of this examiner's answer.

For the above reasons, it is believed that the rejections should be sustained.

Respectfully submitted,

/Marianne P. Allen/

Primary Examiner, Art Unit 1647

Conferees:

/Manjunath N. Rao, /
Supervisory Patent Examiner, Art Unit 1647

Gary Nickol

/Gary B. Nickol /

Supervisory Patent Examiner, Art Unit 1646